

## SEQUENCE LISTING

<110> SUGA, Mikiko  
ASAKURA, Yoko  
MORI, Yukiko  
ITO, Nisao  
KURAHASHI, Osamu

<120> Arginine Repressor Deficient Strain of Coryneform Bacterium and  
Method for Producing L-Arginine

<130> OP1018

<140>

<141> 2001-04-

<150> JP2000-129167

<151> 2000-04-28

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for  
amplifying kanamycin resistant gene of  
Streptococcus faecalis

<400> 1

cccgttaact gcttgaaacc caggacaata ac

<210> 2

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for  
amplifying kanamycin resistant gene of  
*Streptococcus faecalis*

<400> 2

cccgtaaca tgtactcag aaaagattag

30

<210> 3

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for  
amplifying *Escherichia coli* cloning vector pHSG399

<400> 3

gatattctacg tgccgatcaa cgtctc

26

<210> 4

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for  
amplifying *Escherichia coli* cloning vector pHSG399

<400> 4

aggccttttt ttaaggcagt tattg

25

<210> 5

<211> 4447

<212> DNA

<213> *Brevibacterium lactofermentum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1318)..(2598)

&lt;400&gt; 5

aagcttgtct acgtctgatg ctttgaatcg gacggacttg ccgatcttgt atgcggtgat 60  
ttttccctcg ttgcccact ttttaatggt ggccgggggtg agagctacgc gggcggcgac 120  
ctgctgcgct gtgatccaat attcggggtc gttcactggt tcccctttct gatttctggc 180  
atagaagaac ccocgtgaac tgttgtgttc cgggggttgc tgatttttgc gagacttctc 240  
gcgcaattcc ctagcttagg tgaaaacacc atgaaacact agggaaacac ccatgaaaca 300  
cccattaggg cagtagggcg gcttcttcgt ctagggcttg catttgggcg gtgatctggt 360  
ctttagcgtg tgaaaggtg tcgtaggtgg cgtgctcaat gcactcgaaac gtcacgtcat 420  
ttaccgggtc acggtgggca aagagaacta gtgggttaga cattgttttc ctggttgcg 480  
gtggtggtga gcttttctag ccgctcggtg aacgcggcga tcatgaactc ttggaggttt 540  
tcaccgttct gcatgcctgc gcgcttcagt tcctcacgta gtgccaaagg aacgcgtgcg 600  
gtgaccacga cgggcttagc ctttgcctgc gcttctagt cttcgatggt ggcttgtgcc 660  
tgcgcttgct gcgcctgtag tgctgttga gcttcttgta gttgctgttc tagctgtgcc 720  
ttggttgcca tgctttaaga ctctagtagc ttctctgcga tatgtcatgc gcatgcgtag 780  
caaacattgt cctgcaactc attcattatg tgcagtgtc ctgttactag tcgtacatac 840  
tcatatttac ctagtctgca tgcagtgcac gcacatgcag tcatgtcgtg ctaatgtgta 900  
aaacatgtac atgcagattg ctgggggtgc agggggcgga gccacctgt ccatgcgggg 960  
tgtggggctt gcccgcggg tacagacagt gacaccggg gcacctagtc gcggataccc 1020  
cccctaggta tcggacacgt aacctccca tctcgatgca aatctttaac attgagtacg 1080  
ggtaagctgg cagcatagc caagctagc ggccaccaa caccactaaa aattaatagt 1140  
ccctagacaa gacaaacccc cgtgcgagct accaactcat atgcacgggg gccacataac 1200  
ccgaaggggt ttcaattgac aaccatagca ctagctaaga caacgggcac aacacccgca 1260  
caaactcgca ctgcgcaacc ccgcacaaca tcgggtctag gtaacactga aatagaa 1317  
gtg aac acc tct aag gaa ccg cag gtc aat gag ggt tct aag gtc act 1365  
Val Asn Thr Ser Lys Glu Pro Gln Val Asn Glu Gly Ser Lys Val Thr  
1 5 10 15  
cgc gct agg gcg tgg cgt agg caa aac gtc atg tac aag atc acc aat 1413  
Arg Ala Arg Ala Trp Arg Arg Gln Asn Val Met Tyr Lys Ile Thr Asn  
20 25 30  
agt aag gct ctg gcg ggg tgc cat agg tgg cgc agg gac gaa gct gtt 1461  
Ser Lys Ala Leu Ala Gly Cys His Arg Trp Arg Arg Asp Glu Ala Val  
35 40 45  
gcg gtg tcc tgg tgc tct aac ggt gct tgc cag ttt gag ggt ctg caa 1509  
Ala Val Ser Trp Ser Ser Asn Gly Ala Ser Gln Phe Glu Gly Leu Gln  
50 55 60  
aac tct cac tct cgc tgg ggg tca cct ctg gct gaa ttg gaa gtc atg 1557

Asn Ser His Ser Arg Trp Gly Ser Pro Leu Ala Glu Leu Glu Val Met  
 65 70 75 80  
 ggc gaa cgc cgc att gag ctg gct att gct act aag aat cac ttg gcg 1605  
 Gly Glu Arg Arg Ile Glu Leu Ala Ile Ala Thr Lys Asn His Leu Ala  
 85 90 95  
 gcg ggt ggc ggc ctc atg atg ttt gtg ggc act gtt cga cac aac cgc 1653  
 Ala Gly Gly Ala Leu Met Met Phe Val Gly Thr Val Arg His Asn Arg  
 100 105 110  
 tca cag tca ttt ggc cag gtt gaa ggc ggt att aag act gcg tac tct 1701  
 Ser Gln Ser Phe Ala Gln Val Glu Ala Gly Ile Lys Thr Ala Tyr Ser  
 115 120 125  
 tcg atg gtg aaa aca tct cag tgg aag aaa gaa cgt gca cgg tac ggg 1749  
 Ser Met Val Lys Thr Ser Gln Trp Lys Lys Glu Arg Ala Arg Tyr Gly  
 130 135 140  
 gtg gag cac acc tat agt gac tat gag gtc aca gac tct tgg gcg aac 1797  
 Val Glu His Thr Tyr Ser Asp Tyr Glu Val Thr Asp Ser Trp Ala Asn  
 145 150 155 160  
 ggt tgg cac ttg cac cgc aac atg ctg ttg ttc ttg gat cgt cca ctg 1845  
 Gly Trp His Leu His Arg Asn Met Leu Leu Phe Leu Asp Arg Pro Leu  
 165 170 175  
 tct gac gat gaa ctc aag ggc ttt gag gat tcc atg ttt tcc cgc tgg 1893  
 Ser Asp Asp Glu Leu Lys Ala Phe Glu Asp Ser Met Phe Ser Arg Trp  
 180 185 190  
 tct gct ggt gtg gtt aag gcc ggt atg gac ggc cca ctg cgt gag cac 1941  
 Ser Ala Gly Val Val Lys Ala Gly Met Asp Ala Pro Leu Arg Glu His  
 195 200 205  
 ggg gtc aaa ctt gat cag gtg tct acc tgg ggt gga gac gct gcg aaa 1989  
 Gly Val Lys Leu Asp Gln Val Ser Thr Trp Gly Gly Asp Ala Ala Lys  
 210 215 220  
 atg gca acc tac ctc gct aag ggc atg tct cag gaa ctg act ggc tcc 2037  
 Met Ala Thr Tyr Leu Ala Lys Gly Met Ser Gln Glu Leu Thr Gly Ser  
 225 230 235 240  
 gct act aaa acc ggc tct aag ggg tcg tac acg ccg ttt cag atg ttg 2085  
 Ala Thr Lys Thr Ala Ser Lys Gly Ser Tyr Thr Pro Phe Gln Met Leu  
 245 250 255  
 gat atg ttg gcc gat caa agc gac gcc ggc gag gat atg gac gct gtt 2133  
 Asp Met Leu Ala Asp Gln Ser Asp Ala Gly Glu Asp Met Asp Ala Val  
 260 265 270  
 ttg gtg gct cgg tgg cgt gag tat gag gtt ggt tct aaa aac ctg cgt 2181  
 Leu Val Ala Arg Trp Arg Glu Tyr Glu Val Gly Ser Lys Asn Leu Arg  
 275 280 285

tcg tcc tgg tca cgt ggg gct aag cgt gct ttg ggc att gat tac ata 2229  
 Ser Ser Trp Ser Arg Gly Ala Lys Arg Ala Leu Gly Ile Asp Tyr Ile  
 290 295 300  
 gac gct gat gta cgt cgt gaa atg gaa gaa gaa ctg tac aag ctc gcc 2277  
 Asp Ala Asp Val Arg Arg Glu Met Glu Glu Glu Leu Tyr Lys Leu Ala  
 305 310 315 320  
 ggt ctg gaa gca ccg gaa cgg gtc gaa tca acc cgc gtt gct gtt gct 2325  
 Gly Leu Glu Ala Pro Glu Arg Val Glu Ser Thr Arg Val Ala Val Ala  
 325 330 335  
 ttg gtg aag ccc gat gat tgg aaa ctg att cag tct gat ttc gcg gtt 2373  
 Leu Val Lys Pro Asp Asp Trp Lys Leu Ile Gln Ser Asp Phe Ala Val  
 340 345 350  
 agg cag tac gtt cta gat tgc gtg gat aag gct aag gac gtg gcc gct 2421  
 Arg Gln Tyr Val Leu Asp Cys Val Asp Lys Ala Lys Asp Val Ala Ala  
 355 360 365  
 gcg caa cgt gtc gct aat gag gtg ctg gca agt ctg ggt gtg gat tcc 2469  
 Ala Gln Arg Val Ala Asn Glu Val Leu Ala Ser Leu Gly Val Asp Ser  
 370 375 380  
 acc ccg tgc atg atc gtt atg gat gat gtg gac ttg gac gcg gtt ctg 2517  
 Thr Pro Cys Met Ile Val Met Asp Asp Val Asp Leu Asp Ala Val Leu  
 385 390 395 400  
 cct act cat ggg gac gct act aag cgt gat ctg aat gcg gcg gtg ttc 2565  
 Pro Thr His Gly Asp Ala Thr Lys Arg Asp Leu Asn Ala Ala Val Phe  
 405 410 415  
 gcg ggt aat gag cag act att ctt cgc acc cac taaaagcggc ataaaccccg 2618  
 Ala Gly Asn Glu Gln Thr Ile Leu Arg Thr His  
 420 425  
 ttgatattt tgtcgatga atttatggtc aatgtcgcgg gggcaacta tgatgggtct 2678  
 tgtgttgac aatggctgat ttcacagga atggaactgt catgctgita tgtgcctggc 2738  
 tcctaataca agctggggac aatgggttgc cccgttgatc tgatctagtt cggattggcg 2798  
 gggcttcaact gtatctgggg gtggcatcgt gaatagattg cacaccgtag tgggcagtgt 2858  
 gcacaccata gtgggcatga gtaataccta cgcgcgcgtg ggctagggt taacgcgcgt 2918  
 tttgccgtgc tgcgggcat acgttagcgc atacgctttt ttctgtgaaa cctttttgtg 2978  
 ttgttgtttc gtgttggttt cttttctgtt ggcggggcaa cttaacgcct ggcgggggtg 3038  
 ttgttgacgt taacgggggt agtttttatt cccctagtgg tttttcagta cgacaatcga 3098  
 gaaagacctg tttcagccag ttcgggtcat gtctgcgtg atggccacgt gcatagcgac 3158  
 cagttttcga gttcactggg attttttgtg catcgaacaa gatgtaggac aatgcggtt 3218  
 ctaggtctac tttttgcttt atgccgtaca agccccgtgg gtattcagcg attgattcca 3278  
 aggcggettc ccagtcctgt tttgtgaagg actggcttag ttctaggtct gtgtctgggt 3338  
 agtactgctt gtttgtgtaa gcgccgttgg tgctcattga tgattccttt gaagtgtttg 3398  
 gagtccgct agtagtcgg cgtatggtgc tgctttttgc tcgtgatagc tcgccttggc 3458

tatgaggtcg gctaggtagg tttccggggt gcctaggttg cgtaggtcta gcaaattccc 3518  
 gtatgtggcc tgtgcgctgc gctggtggtg catacagtcg ttaagctggg cttttacgtc 3578  
 tggatgcgg tggcggttag gcatgttggt gtgcttcttc caagtactca cgggcggggt 3638  
 ttgttatgc ctggcgtgat gcttctttga gctgttgag ttccgcttg agtgcgggta 3698  
 gtgcgtccgc gaactgcttg tggactcgt atttctcttg ttcctgggcg atagcatttg 3758  
 cgttgaattg cagggcgggt agttcgtcca cgcgtcgttt tgctgcgttg gtcattggtg 3818  
 cgtgccattt gcggttggtg acgcgggggt caaggttgcg cacggctgct tcggctaggt 3878  
 tgggtgctgc ttttttcagt gctcgggctt cccgttcctc gtccaacgag agcacctttg 3938  
 gttgttggtc ttccgctagt ttttgcttct ccgctttgat gagttggtca acttcgtgtt 3998  
 gggagaggtc gtttttcacg atgcgtcgaa tgtggtcgtt gtgggtgctg agttggtgtg 4058  
 agaggtagtg ggttcttggg atttcggcga gttggtcgag gttggtgtag tgcgggttgc 4118  
 ggcttggttg gttggttcg ctggggaggt ccatgtatcc ggttgagtct ccggcgtggt 4178  
 tgaagtgaat taggcgttg tagccgtatt cctggttggg gaggtacgac agaattgagga 4238  
 agtttggtgc ttctcttcca atgagtcgtg cgtgttcgta gttcgttact gggctcgtgct 4298  
 cggggagaat gttcttttgg gtcattgctt ctctttctgt tgctctgtaa gtccgtatgt 4358  
 gggcatggga aagccccggc aaccctttgg gtcaaccggg gctagatagt cgcttagaat 4418  
 ggcttctagg ctgcgtctcg ggggtgtggc 4447

<210> 6

<211> 427

<212> PRT

<213> *Brevibacterium lactofermentum*

<400> 6

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Thr | Ser | Lys | Glu | Pro | Gln | Val | Asn | Glu | Gly | Ser | Lys | Val | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Ala | Arg | Ala | Trp | Arg | Arg | Gln | Asn | Val | Met | Tyr | Lys | Ile | Thr | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Lys | Ala | Leu | Ala | Gly | Cys | His | Arg | Trp | Arg | Arg | Asp | Glu | Ala | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Ser | Trp | Ser | Ser | Asn | Gly | Ala | Ser | Gln | Phe | Glu | Gly | Leu | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Ser | His | Ser | Arg | Trp | Gly | Ser | Pro | Leu | Ala | Glu | Leu | Glu | Val | Met |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Glu | Arg | Arg | Ile | Glu | Leu | Ala | Ile | Ala | Thr | Lys | Asn | His | Leu | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Gly | Gly | Ala | Leu | Met | Met | Phe | Val | Gly | Thr | Val | Arg | His | Asn | Arg |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gln | Ser | Phe | Ala | Gln | Val | Glu | Ala | Gly | Ile | Lys | Thr | Ala | Tyr | Ser |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ser | Met | Val | Lys | Thr | Ser | Gln | Trp | Lys | Lys | Glu | Arg | Ala | Arg | Tyr | Gly |

|   |     |     |
|---|-----|-----|
| 130   | 135 | 140 |
| Val Glu His Thr Tyr Ser Asp Tyr Glu Val Thr Asp Ser Trp Ala Asn |     |     |
| 145   | 150 | 155 |
| Gly Trp His Leu His Arg Asn Met Leu Leu Phe Leu Asp Arg Pro Leu |     | 160 |
|   | 165 | 170 |
| Ser Asp Asp Glu Leu Lys Ala Phe Glu Asp Ser Met Phe Ser Arg Trp |     | 175 |
|   | 180 | 185 |
| Ser Ala Gly Val Val Lys Ala Gly Met Asp Ala Pro Leu Arg Glu His |     | 190 |
|   | 195 | 200 |
| Gly Val Lys Leu Asp Gln Val Ser Thr Trp Gly Gly Asp Ala Ala Lys |     | 205 |
|   | 210 | 215 |
| Met Ala Thr Tyr Leu Ala Lys Gly Met Ser Gln Glu Leu Thr Gly Ser |     | 220 |
| 225   | 230 | 235 |
| Ala Thr Lys Thr Ala Ser Lys Gly Ser Tyr Thr Pro Phe Gln Met Leu |     | 240 |
|   | 245 | 250 |
| Asp Met Leu Ala Asp Gln Ser Asp Ala Gly Glu Asp Met Asp Ala Val |     | 255 |
|   | 260 | 265 |
| Leu Val Ala Arg Trp Arg Glu Tyr Glu Val Gly Ser Lys Asn Leu Arg |     | 270 |
|   | 275 | 280 |
| Ser Ser Trp Ser Arg Gly Ala Lys Arg Ala Leu Gly Ile Asp Tyr Ile |     | 285 |
|   | 290 | 295 |
| Asp Ala Asp Val Arg Arg Glu Met Glu Glu Glu Leu Tyr Lys Leu Ala |     | 300 |
| 305   | 310 | 315 |
| Gly Leu Glu Ala Pro Glu Arg Val Glu Ser Thr Arg Val Ala Val Ala |     | 320 |
|   | 325 | 330 |
| Leu Val Lys Pro Asp Asp Trp Lys Leu Ile Gln Ser Asp Phe Ala Val |     | 335 |
|   | 340 | 345 |
| Arg Gln Tyr Val Leu Asp Cys Val Asp Lys Ala Lys Asp Val Ala Ala |     | 350 |
|   | 355 | 360 |
| Ala Gln Arg Val Ala Asn Glu Val Leu Ala Ser Leu Gly Val Asp Ser |     | 365 |
|   | 370 | 375 |
| Thr Pro Cys Met Ile Val Met Asp Asp Val Asp Leu Asp Ala Val Leu |     | 380 |
| 385   | 390 | 395 |
| Pro Thr His Gly Asp Ala Thr Lys Arg Asp Leu Asn Ala Ala Val Phe |     | 400 |
|   | 405 | 410 |
| Ala Gly Asn Glu Gln Thr Ile Leu Arg Thr His                     |     | 415 |
|   | 420 | 425 |

&lt;210&gt; 7

&lt;211&gt; 4447

&lt;212&gt; DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1318)..(2598)

<400> 7

```

aagcttgctt acgtctgatg ctttgaatcg gacggacttg cegatcttgt atgcggtgat 60
ttttccctcg ttgcccact ttttaatggt ggccggggtg agagctacgc gggcggcgac 120
ctgctgcgct gtgatccaat attcggggtc gttcactggt tcccctttct gatttctggc 180
atagaagaac ccccgtagac tgtgtggttc cgggggttgc tgatttttgc gagacttctc 240
gcgcaattcc ctagcttagg tgaaaacacc atgaaacact agggaaacac ccatgaaaca 300
cccattaggg cagtagggcg gcttcttcgt ctagggcttg catttgggcg gtgatctggt 360
ctttagcgtg tgaaagtgtg tcgtaggttg cgtgctcaat gcactcgaac gtcacgtcat 420
ttaccgggtc acggtgggca aagagaacta gtgggttaga cattgttttc ctggttgctg 480
gtggtggtga gcttttctag ccgctcggtg aacgcggcga tcatgaactc ttggagggtt 540
tcaccgttct gcatgcctgc gcgcttcatt tcctcacgta gtgccaaagg aacgcgtgcg 600
gtgaccacga cgggcttagc ctttgcttgc gcttctagt cttcgatggt ggcttgtgcc 660
tgcgcttgct gcgcctgtag tgccctgtga gcttcttgta gttgctgttc tagctgtgcc 720
ttggttgcca tgctttaaga ctctagtagc tttctcgga tatgtcatgc gcatgcgtag 780
caaacattgf cctgcaactc attcattatg tgcagtgtc ctgttactag tcgtacatac 840
tcataattac ctagtctgca tgcagtgcac gcacatgcag tcatgtcgtg ctaatgtgta 900
aaacatgtac atgcagattg ctgggggtgc agggggcgga gccacctgt ccatgcgggg 960
tgtggggctt gccccgcggg tacagacagt gaggaccggg gcacctagtc gcggataccc 1020
cccctaggta tcggacacgt aacctccca tgcgatgca aatctttaac attgagtacg 1080
ggtaagctgg cagcatagc caagctaggc ggccaccaa caccactaaa aattaatagt 1140
tctagacaa gacaaacccc cgtgcgagct accaactcat atgcacgggg gccacataac 1200
ccgaaggggt ttcaattgac aaccatagca ctagctaaga caacgggcac aacatccgca 1260
caaactcgca ctgcgcaacc ccgcacaaca tcgggtctag gtaacactga aatagaa 1317
gtg aac acc tct aag gaa ccg cag gtc aat gag ggt tct aag gtc act 1365
Val Asn Thr Ser Lys Glu Pro Gln Val Asn Glu Gly Ser Lys Val Thr
      1             5             10             15
cgc gct agg gcg tgg cgt agg caa aac gtc atg tac aag atc acc aat 1413
Arg Ala Arg Ala Trp Arg Arg Gln Asn Val Met Tyr Lys Ile Thr Asn
      20             25             30
agt aag gct ctg gcg ggg tgc cat agg tgg cgc agg gac gaa gct gtt 1461
Ser Lys Ala Leu Ala Gly Cys His Arg Trp Arg Arg Asp Glu Ala Val
      35             40             45
gcg gtg tcc tgg tgc tct aac ggt gct tgc cag ttt gag ggt ctg caa 1509
Ala Val Ser Trp Ser Ser Asn Gly Ala Ser Gln Phe Glu Gly Leu Gln
      50             55             60

```



aac tct cac tct cgc tgg ggg tca tct ctg gct gaa ttg gaa gtc atg 1557  
 Asn Ser His Ser Arg Trp Gly Ser Ser Leu Ala Glu Leu Glu Val Met  
 65 70 75 80  
 ggc gaa cgc cgc att gag ctg gct att gct act aag aat cac ttg gcg 1605  
 Gly Glu Arg Arg Ile Glu Leu Ala Ile Ala Thr Lys Asn His Leu Ala  
 85 90 95  
 gcg ggt ggc gcg ctc atg atg ttt gtg ggc act gtt cga cac aac cgc 1653  
 Ala Gly Gly Ala Leu Met Met Phe Val Gly Thr Val Arg His Asn Arg  
 100 105 110  
 tca cag tca ttt ggc cag gtt gaa gcg ggt att aag act gcg tac tct 1701  
 Ser Gln Ser Phe Ala Gln Val Glu Ala Gly Ile Lys Thr Ala Tyr Ser  
 115 120 125  
 tcg atg gtg aaa aca tct cag tgg aag aaa gaa cgt gca cgg tac ggg 1749  
 Ser Met Val Lys Thr Ser Gln Trp Lys Lys Glu Arg Ala Arg Tyr Gly  
 130 135 140  
 gtg gag cac acc tat agt gac tat gag gtc aca gac tct tgg gcg aac 1797  
 Val Glu His Thr Tyr Ser Asp Tyr Glu Val Thr Asp Ser Trp Ala Asn  
 145 150 155 160  
 ggt tgg cac ttg cac cgc aac atg ctg ttg ttc ttg gat cgt cca ctg 1845  
 Gly Trp His Leu His Arg Asn Met Leu Leu Phe Leu Asp Arg Pro Leu  
 165 170 175  
 tct gac gat gaa ctc aag gca ttt gag gat tcc atg ttt tcc cgc tgg 1893  
 Ser Asp Asp Glu Leu Lys Ala Phe Glu Asp Ser Met Phe Ser Arg Trp  
 180 185 190  
 tct gct ggt gtg gtt aag gcc ggt atg gac gcg cca ctg cgt gag cac 1941  
 Ser Ala Gly Val Val Lys Ala Gly Met Asp Ala Pro Leu Arg Glu His  
 195 200 205  
 ggg gtc aaa ctt gat cag gtg tct acc tgg ggt gga gac gct gcg aaa 1989  
 Gly Val Lys Leu Asp Gln Val Ser Thr Trp Gly Gly Asp Ala Ala Lys  
 210 215 220  
 atg gca acc tac ctc gct aag ggc atg tct cag gaa ctg act ggc tcc 2037  
 Met Ala Thr Tyr Leu Ala Lys Gly Met Ser Gln Glu Leu Thr Gly Ser  
 225 230 235 240  
 gct act aaa acc gcg tct aaa ggg tcg tac acg ccg ttt cag atg ttg 2085  
 Ala Thr Lys Thr Ala Ser Lys Gly Ser Tyr Thr Pro Phe Gln Met Leu  
 245 250 255  
 gat atg ttg gcc gat caa agc gac gcc ggc gag gat atg gac gct gtt 2133  
 Asp Met Leu Ala Asp Gln Ser Asp Ala Gly Glu Asp Met Asp Ala Val  
 260 265 270  
 ttg gtg gct cgg tgg cgt gag tat gag gtt ggt tct aaa aac ctg cgt 2181  
 Leu Val Ala Arg Trp Arg Glu Tyr Glu Val Gly Ser Lys Asn Leu Arg

275 280 285  
 tct tct tgg tca cgt ggg gct aag cgt gct ttg ggc att gat tac ata 2229  
 Ser Ser Trp Ser Arg Gly Ala Lys Arg Ala Leu Gly Ile Asp Tyr Ile  
 290 295 300  
 gac gct gat gta cgt cgt gaa atg gaa gaa gaa ctg tac aag ctc gcc 2277  
 Asp Ala Asp Val Arg Arg Glu Met Glu Glu Glu Leu Tyr Lys Leu Ala  
 305 310 315 320  
 ggt ctg gaa gca ccg gaa cgg gtc gaa tca acc cgc gtt gct gtt gct 2325  
 Gly Leu Glu Ala Pro Glu Arg Val Glu Ser Thr Arg Val Ala Val Ala  
 325 330 335  
 ttg gtg aag ccc gat gat tgg aaa ctg att cag tct gat ttc gcg gtt 2373  
 Leu Val Lys Pro Asp Asp Trp Lys Leu Ile Gln Ser Asp Phe Ala Val  
 340 345 350  
 agg cag tac gtt cta gat tgc gtg gat aag gct aag gac gtg gcc gct 2421  
 Arg Gln Tyr Val Leu Asp Cys Val Asp Lys Ala Lys Asp Val Ala Ala  
 355 360 365  
 gcg caa cgt gtc gct aat gag gtg ctg gca agt ctg ggt gtg gat tcc 2469  
 Ala Gln Arg Val Ala Asn Glu Val Leu Ala Ser Leu Gly Val Asp Ser  
 370 375 380  
 acc ccg tgc atg atc gtt atg gat gat gtg gac ttg gac gcg gtt ctg 2517  
 Thr Pro Cys Met Ile Val Met Asp Asp Val Asp Leu Asp Ala Val Leu  
 385 390 395 400  
 cct act cat ggg gac gct act aag cgt gat ctg aat gcg gcg gtg ttc 2565  
 Pro Thr His Gly Asp Ala Thr Lys Arg Asp Leu Asn Ala Ala Val Phe  
 405 410 415  
 gcg ggt aat gag cag act att ctt cgc acc cac taaaagcggc ataaaccccg 2618  
 Ala Gly Asn Glu Gln Thr Ile Leu Arg Thr His  
 420 425  
 ttgatattt tgtcgatga atttatggtc aatgtcgagg gggcaaacta tgatgggtct 2678  
 tgttgttgac aatggctgat ttcatcagga atggaactgt catgctgtta tgtgcctggc 2738  
 tcctaataca agctggggac aatgggttgc ccggttgatc tgatctagtt cggattggcg 2798  
 gggcttcact gtatctgggg gtggcatcgt gaatagattg cacacgtag tgggcagtgt 2858  
 gcacaccata gtgggcatga gtaataccta cgcgcgcgtg ggctagggt taacgcgcgt 2918  
 tttgcggtgc tgcggggcat acgttagcgc atacgctttt ttctgtgaaa cctttttgtg 2978  
 ttgttgtttc gtgttggttt cttttctgtt ggccggggcaa cttaacgcct gcgggggttg 3038  
 ttgttgacgt taacgggggt agtttttatt ccctagtggt tttttcagta agacaatcga 3098  
 gaaagacctg tttcagccag ttccgggtcat gtccgtcggt atggccacgt gcatagcgac 3158  
 cagttttcga gttcactggg attttttggt catcaaaca gatgtaggac aatggggttt 3218  
 ctaggctctac tttttgcttt atgccgtaca agccccgtgg gtattcagcg attgattcca 3278  
 aggcggcttc ccagtcctgt tttgtgaagg actggcttag ttctaggtct gtgtctgggt 3338  
 agtactgctt gtttgtgtaa gcgcggttg tgctcattga tgattccttt gaagtgtttg 3398

gagttcggct agtagtgcgg cgtatggtgc tgctttttgc tcgtgatagc tcgccttggc 3458  
 tatgaggtcg gctaggtagg ttccgggggt gcctaggttg cgtaggtcta gcaaattccc 3518  
 gtatgtggcc tgtgcgctgc gctggtggtg catacagtcg ttaagctggg cttttacgtc 3578  
 tgcgatgcgg tggcggtagt gcatgttggt gtgcttcttc caagtactca cgggcggggt 3638  
 ttgtgtatgc ctggcgtagt gcttctttga gctgttggag ttccgcttgg agtgcgggta 3698  
 gttcgtccgc gaactgcttg tggtagctgt atttctcttg ttccgtggcg atagcatttg 3758  
 cgttgaattg cagggcggtg agttcgtcca cgcgtcgttt tgctgcgttg gtcattggtg 3818  
 cgtgccattt gcggttgttg acgcgggggt caaggttgcg cacggctgct tcggctaggt 3878  
 tggtagctgc ttttttcagt gctcgggctt cccgttcttc gtccaacgag agcacctttg 3938  
 gtttgttggc ttccgctagt ttttgcttct ccgctttgat gagttggtca acttcgtgtt 3998  
 gggagaggtc gtttttcacg atgcgtcgaa tgggtcgtt gtgggtgctg agttggtgtg 4058  
 agaggtagtg gggttctcgg atttcggcga gttggtcgag gttggtgtag tgcgggttgc 4118  
 ggcttggttg gttgggttcg ctggggaggt cgatgtatcc ggttgagtct ccggcgtggt 4178  
 tgaagtgaat taggcgttg tagccgtatt cctggttggg gaggtacgac agaattgagga 4238  
 agtttgggtc ttctctcga atgagtcgtg cgtgttcgta gttcgttact gggctcgtgct 4298  
 cggggagaat gttcttttgg gtcattgctt ctctttctgt tgctctgtaa gtccgtatgt 4358  
 gggcatggga aagccccggc aacccttttg gtcaaccggg gctagatagt cgcttagaat 4418  
 ggcttctagg ctgcgtctcg ggggtggtc 4447

<210> 8

<211> 427

<212> PRT

<213> *Brevibacterium lactofermentum*

<400> 8

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Thr | Ser | Lys | Glu | Pro | Gln | Val | Asn | Glu | Gly | Ser | Lys | Val | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Ala | Arg | Ala | Trp | Arg | Arg | Gln | Asn | Val | Met | Tyr | Lys | Ile | Thr | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Lys | Ala | Leu | Ala | Gly | Cys | His | Arg | Trp | Arg | Arg | Asp | Glu | Ala | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Ser | Trp | Ser | Ser | Asn | Gly | Ala | Ser | Gln | Phe | Glu | Gly | Leu | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Ser | His | Ser | Arg | Trp | Gly | Ser | Ser | Leu | Ala | Glu | Leu | Glu | Val | Met |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Glu | Arg | Arg | Ile | Glu | Leu | Ala | Ile | Ala | Thr | Lys | Asn | His | Leu | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Gly | Gly | Ala | Leu | Met | Met | Phe | Val | Gly | Thr | Val | Arg | His | Asn | Arg |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Ser | Gln | Ser | Phe | Ala | Gln | Val | Glu | Ala | Gly | Ile | Lys | Thr | Ala | Tyr | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Ser Met Val Lys Thr Ser Gln Trp Lys Lys Glu Arg Ala Arg Tyr Gly  
 130 135 140  
 Val Glu His Thr Tyr Ser Asp Tyr Glu Val Thr Asp Ser Trp Ala Asn  
 145 150 155 160  
 Gly Trp His Leu His Arg Asn Met Leu Leu Phe Leu Asp Arg Pro Leu  
 165 170 175  
 Ser Asp Asp Glu Leu Lys Ala Phe Glu Asp Ser Met Phe Ser Arg Trp  
 180 185 190  
 Ser Ala Gly Val Val Lys Ala Gly Met Asp Ala Pro Leu Arg Glu His  
 195 200 205  
 Gly Val Lys Leu Asp Gln Val Ser Thr Trp Gly Gly Asp Ala Ala Lys  
 210 215 220  
 Met Ala Thr Tyr Leu Ala Lys Gly Met Ser Gln Glu Leu Thr Gly Ser  
 225 230 235 240  
 Ala Thr Lys Thr Ala Ser Lys Gly Ser Tyr Thr Pro Phe Gln Met Leu  
 245 250 255  
 Asp Met Leu Ala Asp Gln Ser Asp Ala Gly Glu Asp Met Asp Ala Val  
 260 265 270  
 Leu Val Ala Arg Trp Arg Glu Tyr Glu Val Gly Ser Lys Asn Leu Arg  
 275 280 285  
 Ser Ser Trp Ser Arg Gly Ala Lys Arg Ala Leu Gly Ile Asp Tyr Ile  
 290 295 300  
 Asp Ala Asp Val Arg Arg Glu Met Glu Glu Glu Leu Tyr Lys Leu Ala  
 305 310 315 320  
 Gly Leu Glu Ala Pro Glu Arg Val Glu Ser Thr Arg Val Ala Val Ala  
 325 330 335  
 Leu Val Lys Pro Asp Asp Trp Lys Leu Ile Gln Ser Asp Phe Ala Val  
 340 345 350  
 Arg Gln Tyr Val Leu Asp Cys Val Asp Lys Ala Lys Asp Val Ala Ala  
 355 360 365  
 Ala Gln Arg Val Ala Asn Glu Val Leu Ala Ser Leu Gly Val Asp Ser  
 370 375 380  
 Thr Pro Cys Met Ile Val Met Asp Asp Val Asp Leu Asp Ala Val Leu  
 385 390 395 400  
 Pro Thr His Gly Asp Ala Thr Lys Arg Asp Leu Asn Ala Ala Val Phe  
 405 410 415  
 Ala Gly Asn Glu Gln Thr Ile Leu Arg Thr His  
 420 425

&lt;210&gt; 9

&lt;211&gt; 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for  
introducing mutation to pAM330

<400> 9

aaacccgggc tacgtctgat gctttgaatc

30

<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for  
introducing mutation to pAM330

<400> 10

tttgatcccc cgtaaagtc aacaacc

27

<210> 11

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for  
introducing mutation to pAM330

<400> 11

ttttcccgga agcttgccac accccgag

28

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for  
introducing mutation to pAM330

<400> 12  
gggggtcatc tctggctgaa ttgg 24

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for  
introducing mutation to pAM330

<400> 13  
gaggttttca cgttctgca tgcc 24

<210> 14  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for  
introducing mutation to pAM330

<400> 14  
aactcacgcg cctgcaattc aac 23

<210> 15  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for PCR

<400> 15  
gcctaccgcg gcaaagaagt ggcag 25

<210> 16  
<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for PCR

<400> 16

gccttgaact aggggcgctt taagt

25

<210> 17

<211> 4235

<212> DNA

<213> Brevibacterium flavum

<220>

<221> CDS

<222> (1852)..(2364)

<400> 17

aaaccgggt tttcttctgc aactcgggc ccgaagcaaa cgaggctgct ttcaagattg 60  
cacgcttgac tggctgttcc cggattctgg ctgcagttca tggtttccac ggccgcacca 120  
tgggttcct cgcgtgact ggccagccag acaagcgtga agcgttctg ccaatgccaa 180  
gcggtgtgga gttctaccct tacggcgaca ccgattactt gcgcaaaatg gtagaaacca 240  
acccaacgga tgtggtgct atcttctctg agccaatcca gggtgaaacg ggctgtgttc 300  
cagcacctga aggattcctc aaggcagtgc gcgagctgtg cgatgagtac ggcatcttga 360  
tgatcaccca tgaagtccag actggcgctg gccgtaccgg cgatttcttt gcacatcagc 420  
acgatggcgt tgttcccgat gtggtgacca tggccaaggg acttggcggc ggtcttccca 480  
tcggtgcttg tttggccact ggccgtgcag ctgaattgat gacccagcgc aagcaacgca 540  
ccactttcgg tggcaaccca gttgcttgtg cagctgcca ggcagtgctg tctgttgtcg 600  
atgacgcttt ctgcgcagaa gttaccgcga agggcgagct gttcaaggta cttcttgcca 660  
aggttgacgg cgtttagtag gtcctggca gggccttgat gttggcgctg gtgctggagc 720  
gcgacgtcgc aaagcaagct gttcttgatg gttttaagca cggcgttatt ttgaatgcac 780  
cggcgacaaa cattatccgt ttgacccgc cgttggtgat caccgacgaa gaaatcgagc 840  
acgcagtcaa ggctattgcc gagacaatcg cataaaggac ttaaacttat gacttcacaa 900  
ccacaggttc gccatttctt ggctgatgat gatctcacc ctgcagagca ggcagaggtt 960  
ttgaccctag ccgcaaagct caaggcagcg ccgttttcgg agcgtccact cgagggacca 1020  
aagtccgttg cagttctttt tgataagact tcaactcgta ctgcttctc cttcgacgcg 1080  
ggcatcgctc atttgggtgg acatgccatc gtcgtggatt ccggcagctc acagatgggt 1140  
aagggcgaga ccctgcagga caccgcagct gtattgtccc gctacgtgga agcaattgtg 1200  
tggcgcacct acgcacacag caatttccac gccatggcgg agacgtccac tgtgccgctg 1260  
tgtaactcct tgtccgatga tctgcaccca tgccagattc tggctgatct gcagaccatc 1320

gtggaaaacc tcagccctga agaaggccca gcaggcctta agggtaagaa ggctgtgtac 1380  
 ctgggcgatg gcgacaacaa catggccaac tcctacatga ttggctttgc caccgcgggc 1440  
 atggatattt ccatcatcgc tctgaaggg ttccagcctc gtgcggaatt cgtggagcgc 1500  
 gcgaaaagc gtggccagga aaccggcgcg aaggttgtg tcaccgacag cctcgacgag 1560  
 gttgccgcg ccgatgttgt catcacgat acctgggtat ccatgggtat ggaaaacgac 1620  
 ggcacgac gcaccacacc ttctgttctt taccaggtca acgatgaggt catggcgaaa 1680  
 gctaacgacg gcgccatctt cctgcactgc cttcctgcct accgcggcaa agaagtggca 1740  
 gcctccgtga ttgatggacc agcgtccaaa gttttcgatg aagcagaaaa ccgcctccac 1800  
 gtcagaaaag cactgctggt gtggctgctg gccaccacgc cgaggtaaga c atg tct 1857

Met Ser

1

ctt ggc tca acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc 1905  
 Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg

5

10

15

act gca cgc caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc 1953  
 Thr Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val

20

25

30

acc agc cag gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat 2001  
 Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp

35

40

45

50

atc acc cag gcc acc ttg tcc cgg gat ctc gat gaa ctc ggt gca cgc 2049  
 Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg

55

60

65

aag gtt cgc ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta 2097  
 Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val

70

75

80

gat agc atc gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc 2145  
 Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg

85

90

95

cgc atg ctt gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc 2193  
 Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile

100

105

110

gcg atg ctg cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc 2241  
 Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe

115

120

125

130

atc gat agg gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggc gat 2289  
 Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp

135

140

145

gac acc gtt ttt gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta 2337  
 Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu

150

155

160



ggt gaa tta ctc agc ggg cgc acc act taaagcgccc ctagttcaag 2384  
 Gly Glu Leu Leu Ser Gly Arg Thr Thr

165

170

gcttgttaat cgtttgttaa tgcaggcagg taaggataaa cccgagtgtt ttttcgagga 2444  
 ataccaacc tttcaacaca ataattttct ttaaaccatcc ttgctgtcca ccacggctgg 2504  
 caaggaactt aaaatgaagg agcacacctc atgactaacc gcacgttct tgcatactcc 2564  
 ggcggtcttg acaccactgt ggcaattcca tacctgaaga agatgattga tggatgaagtc 2624  
 atcgagttt cttcgcacct gggccagggt ggagagaaca tggacaacgt tgcgcagcgt 2684  
 gcattggatg ccgtgcagc tgagtcacat gttgttgatg caaaggatga gttcgtgag 2744  
 gagtactgcc tgccaacat caaggcaaac ggcatgtaca tgaagcagta cccactggtt 2804  
 tctgcaatct cccgccact gatcgtcaag cacctcgttg aggctggcaa gcagttcaac 2864  
 ggtaccacag ttgcacagg ctgcactggt aagggaacg accaggttcg tttcgaggtc 2924  
 ggcttcatgg acaccgatcc aaacctggag atcattgcac ctgctcgtga cttcgcagtg 2984  
 acccgcgaca aggctatcgc cttcgccgag gagaacaacg ttccaatcga gcagtcctg 3044  
 aagtcgccat tctccatcga ccagaacgtc tggggccgag ctattgagac cgtttacctg 3104  
 gaagatctgt ggaatgctc aaccaaggac atctacgcat acaccgagga tccagctctg 3164  
 ggtaacgctc cagatgaggt catcatctcc ttcgagggtg gcaagccagt ctccatcgat 3224  
 ggccgtccag tctccgtact gcaggtatg gaagagctga accgtcgtgc aggcgcacag 3284  
 ggcttggcc gccttgacat ggttgaggac cgtctcgttg gcacaaagtc ccgcgaaatc 3344  
 tacgaagcac caggcgcaat cgcactgatt aaggctcacg aggctttgga agatgtcacc 3404  
 atcgagcgcg aactggctcg ctacaagcgt ggcttgacg cacgttgggc tgaggaagta 3464  
 tacgacggcc tgtggttcgg acctctgaag cgctccctgg acgcttcat tgattccacc 3524  
 caggagcacg tcaccggcga tatccgatg gttctgcacg caggttccat caccatcaat 3584  
 ggtcgtcgtt ccagccactc cctgtacgac ttcaacctgg ctacctacga caccggcgac 3644  
 accttcgacc agacctggc taagggttt gtccagctgc acggtctgtc ctccaagatc 3704  
 gctaacaagc gcgatcgga agctggcaac aactaagcca cttttcaag catccagact 3764  
 agaacttcaa gtatttagaa agtagaagaa caccacatgg aacagcacgg aaccaatgaa 3824  
 ggtgcgctgt ggggcggccg cttctccggt ggacctccg aggccatgtt cgccttgagt 3884  
 gtctccactc atttcgactg ggttttggcc ctttatgatg tgttggcctc caaggcacac 3944  
 gccaaggttt tgcaccaagc agagctactt tctgatgaag atctagccac catgctggct 4004  
 ggtcttgatc agctgggcaa ggatgtcgcc gacggaacct tcggtccgct gccttctgat 4064  
 gaggatgtgc acggcgcat ggaacgcgt ctgattgacc gcgttggtcc tgagggtggc 4124  
 ggccgtctgc gcgtggctg ttcccgaac gaccaggtgg caacctgtt ccgcatgtgg 4184  
 gtccgcgacg cagtgcgga catcgctg ggaacaaccg agcttctga c 4235

&lt;210&gt; 18

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Brevibacterium flavum

&lt;400&gt; 18

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val  
 1 5 10 15  
 Thr Arg Thr Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln  
 20 25 30  
 Lys Val Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly  
 35 40 45  
 Ile Asp Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly  
 50 55 60  
 Ala Arg Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly  
 65 70 75 80  
 Pro Val Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys  
 85 90 95  
 Leu Arg Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly  
 100 105 110  
 Asn Ile Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala  
 115 120 125  
 Ser Phe Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala  
 130 135 140  
 Gly Asp Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys  
 145 150 155 160  
 Glu Leu Gly Glu Leu Leu Ser Gly Arg Thr Thr  
 165 170

<210> 19

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for PCR

<400> 19

cccggtttt cttctgcaac tcggg

25

<210> 20

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for PCR

<400> 20

gtcgacaagc tcggttggtc ccagc

25

<210> 21

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for PCR

<400> 21

cccctagttc aaggcttggtt aatc

24

<210> 22

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for PCR

<400> 22

gtcttacctc ggctggttgg ccagc

25